

```

0      10      20      30      40      50      60      70      80      90
GTC TAC ATG GGT GCT TCC CAT TCC AGG GAT GAG CTAC CTG TGG GCT CGT ACAC AGG GACT TGG CCG CTG CGA ACG TGT GGT CAAG AGT CC
Gly Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Ser Pro

100    CAACC ATGT CAAA ATTAC AGACT TCGGG CTGG CTGG TGG ACATTG ACG AGAC AGAGT ACC ATGC AGATGG GGG CCA AGG TTAG GTGA AGG ACCA AG
oAsn His Val Lys Ile Thr Asp Phe Gly Leu Ala Arg Leu Ile Asp Glu Thr Glu Tyr His Ala Asp Gly Gly Lys

200    GAGC AGAGG AGG CTGG GTGG AGTGG TGTCTAG CCCC ATGGG AGAACTCTG AGTGG CCCC ACCCTCCC CACACAC ACAGT TGGAGG ACTTCC TCTTCTG CCCC TC

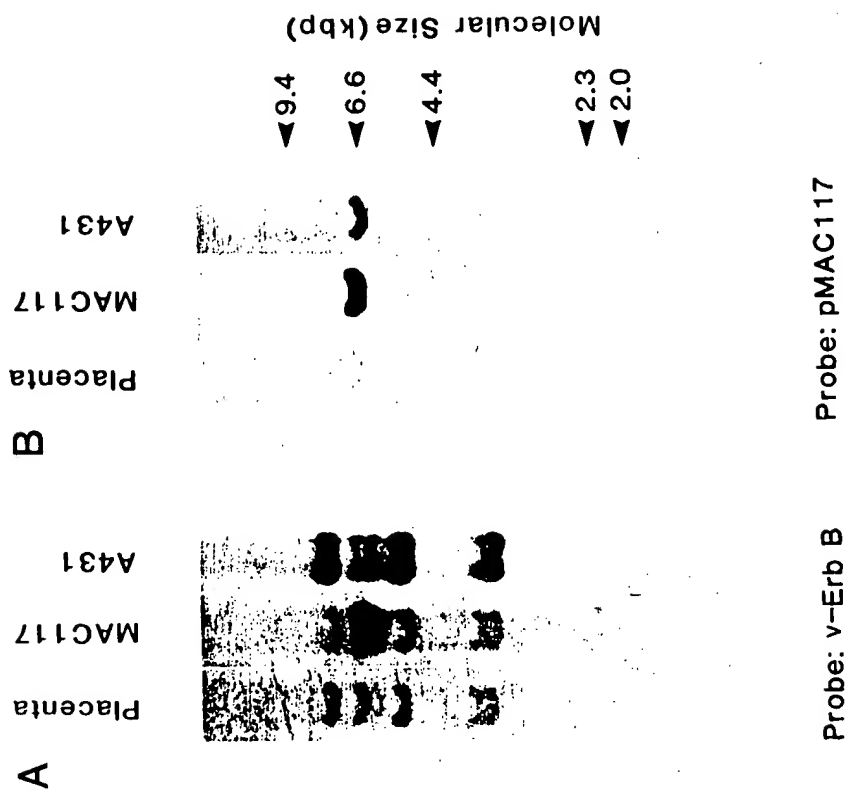
300    CCAG GTGCC CATCA AGTGG ATGG CGCTGG AGTCC ATTCTCC GCGCG GCGG TTCAC CCAC CAGAGT GATGT GTGG AGTTAT GGTGTG TATGG TGGGG GTGTTG
Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly

400    GGAG GGTGG GTGAG GGC CATGG

```

FIG. 1

FIG. 2



# SEQUENCE COMPARISON WITH TYROSINE KINASE PROTEINS

	Homology	
pMAC117		* ** * * *
Human EGF R	85%	GMSYLEDVRLVHRDLAARNVLKSPNHVKITDFGLARLLDI
v-erb B	85%	N R T Q T Q K GA
v-src	52%	N ER T Q T Q K GA
v-abl	51%	A V RMNY R A I GENLVC VA I--
v-fms	50%	A E KKNFI C GENHL VA S MTG
Human Insulin R	42%	A F ASKNCI V LT GRVA G DI-M
		A NAKKF CM AHDFT G MS DT--

	Homology	
pMAC117		* * * * *
Human EGF R		DETEYHA-DG-GK--VPIKWMALLESILRRRFTHQSDVWSYGV
v-erb B		E K E E H IY H IY
v-src		EDN T RQ T P AA YG IK
v-abl		TYTA - A F F T P LAYNK SIK F I
v-fms		NDSN IV K NAR L V P FDCVY V AF
Human Insulin Receptor		Y TD YR K GLL VR P LKDGV TS M F

FIG. 3

110791

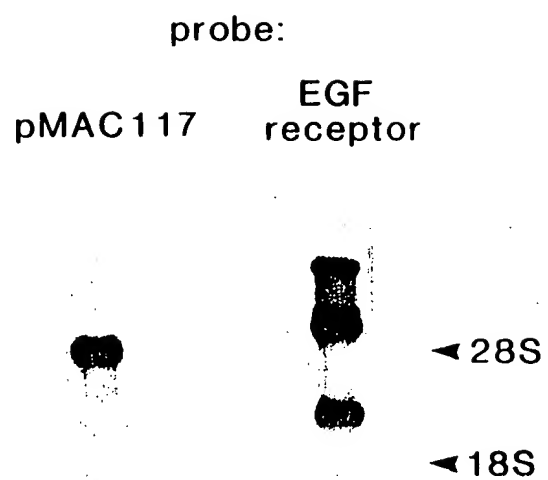
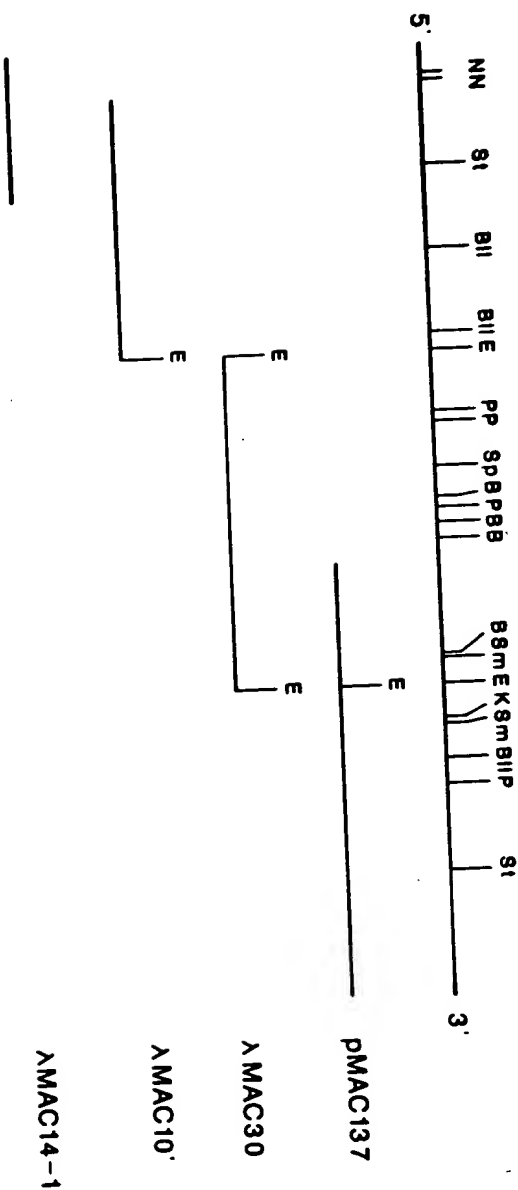
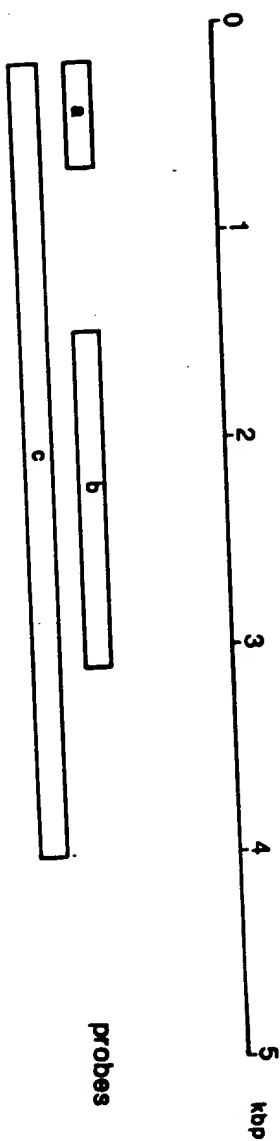


FIG. 4

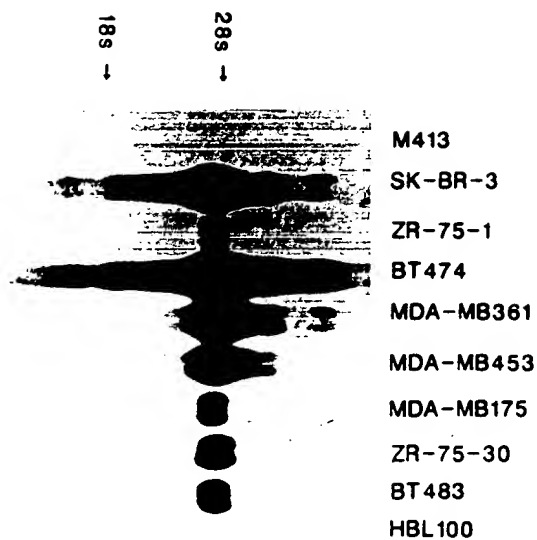
A



B



A



B

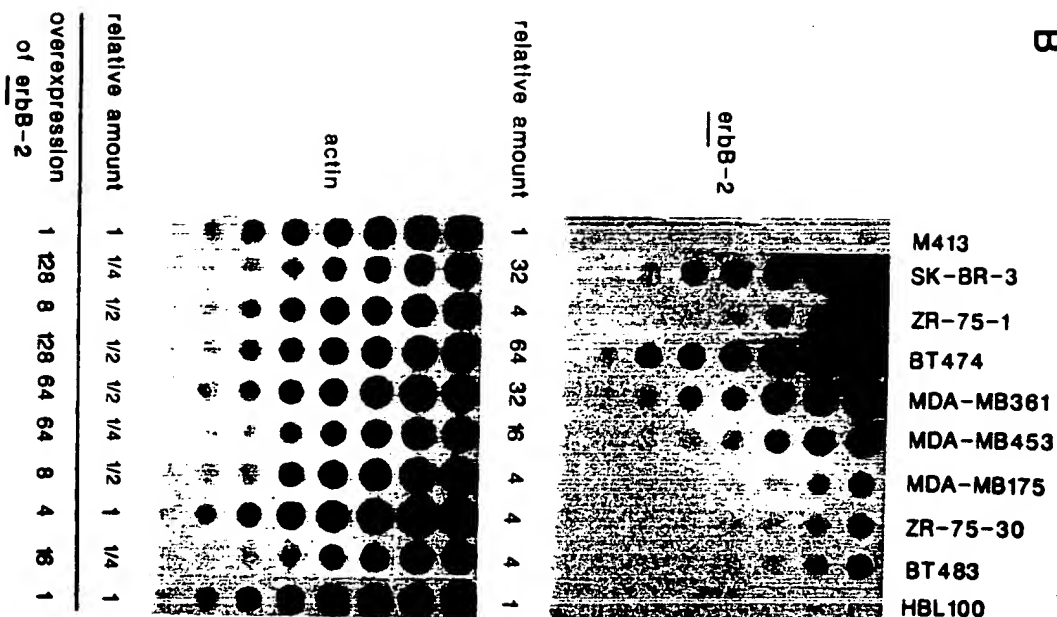
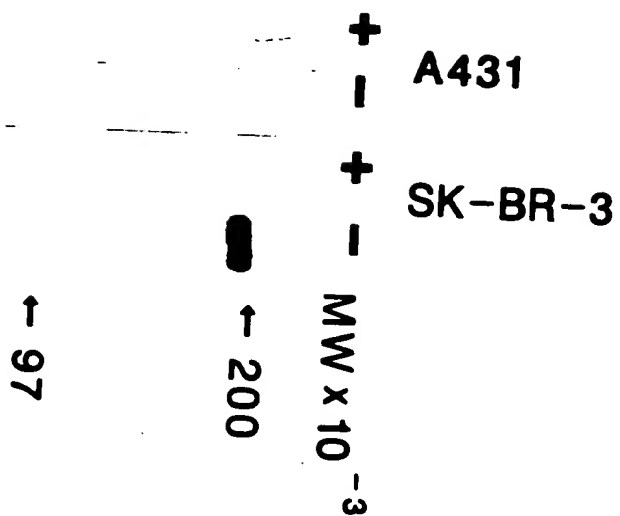


Figure 7

A



B

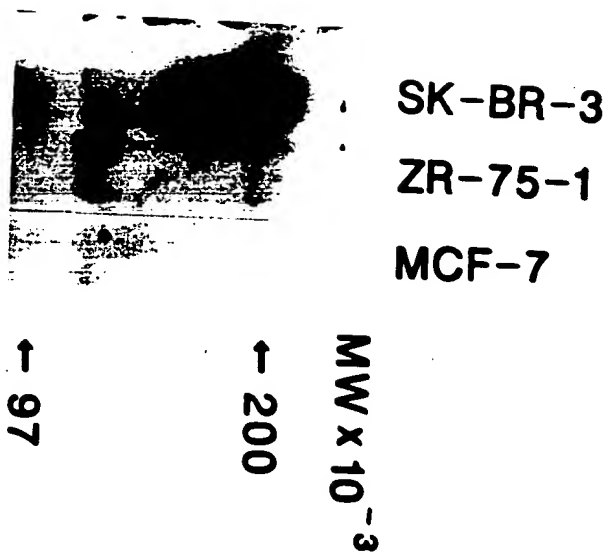


Figure 8

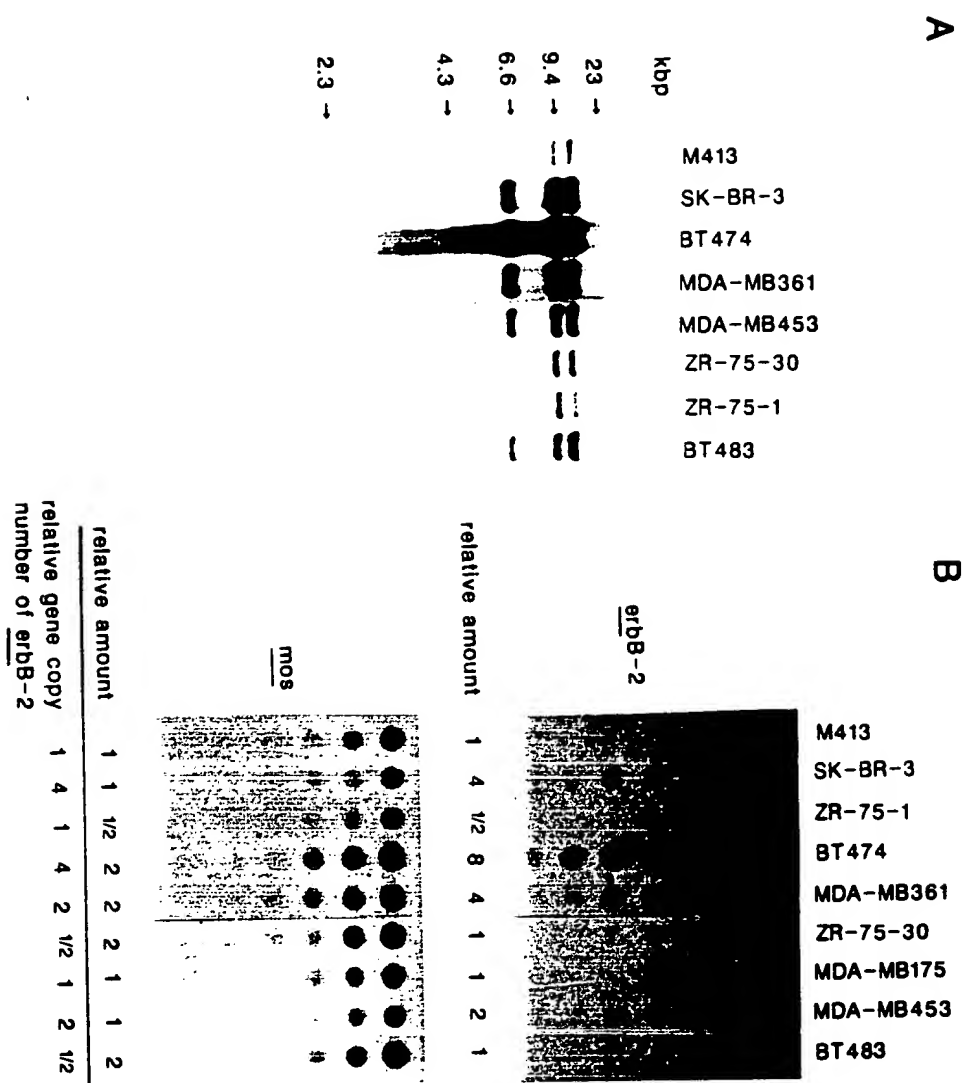
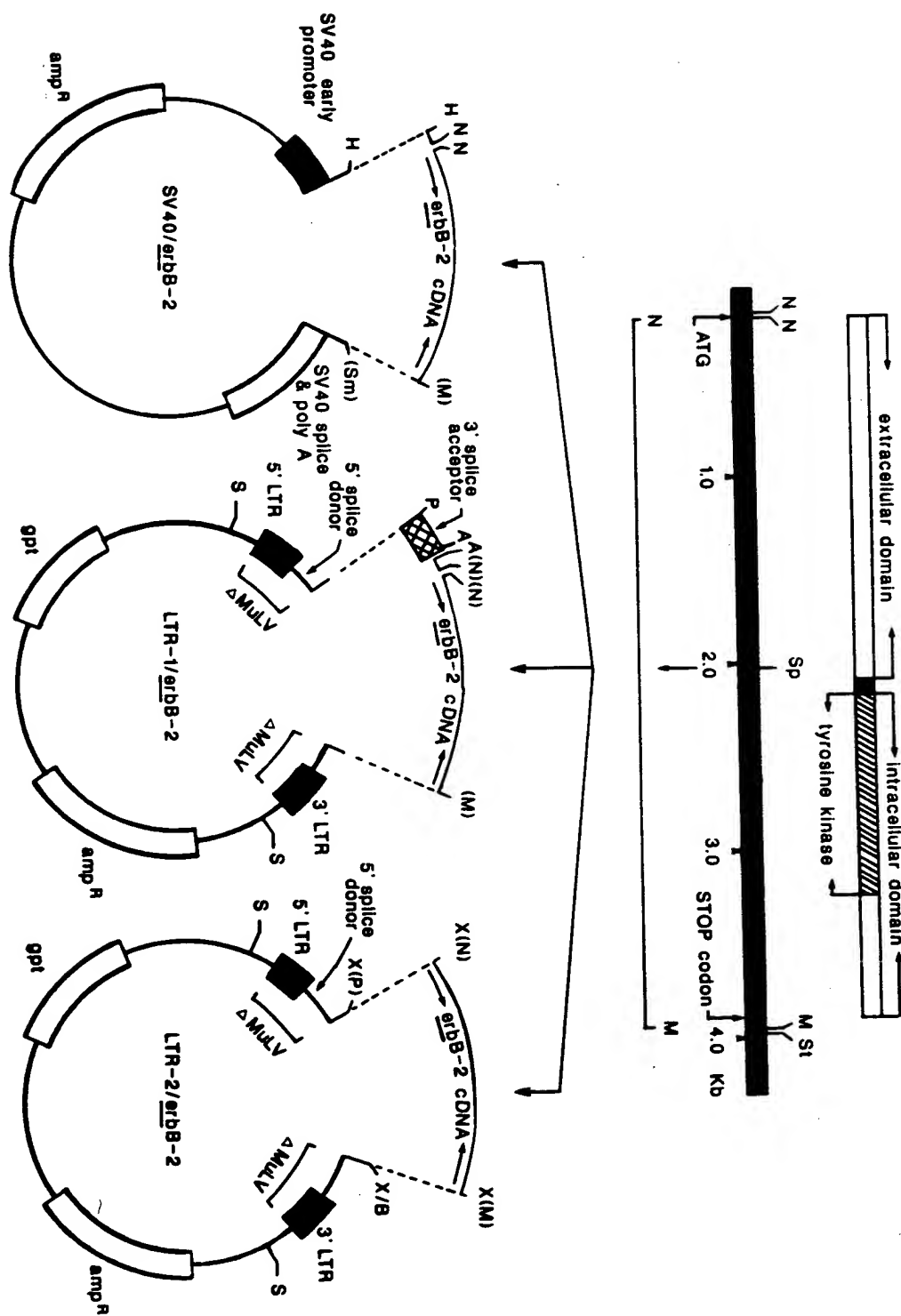
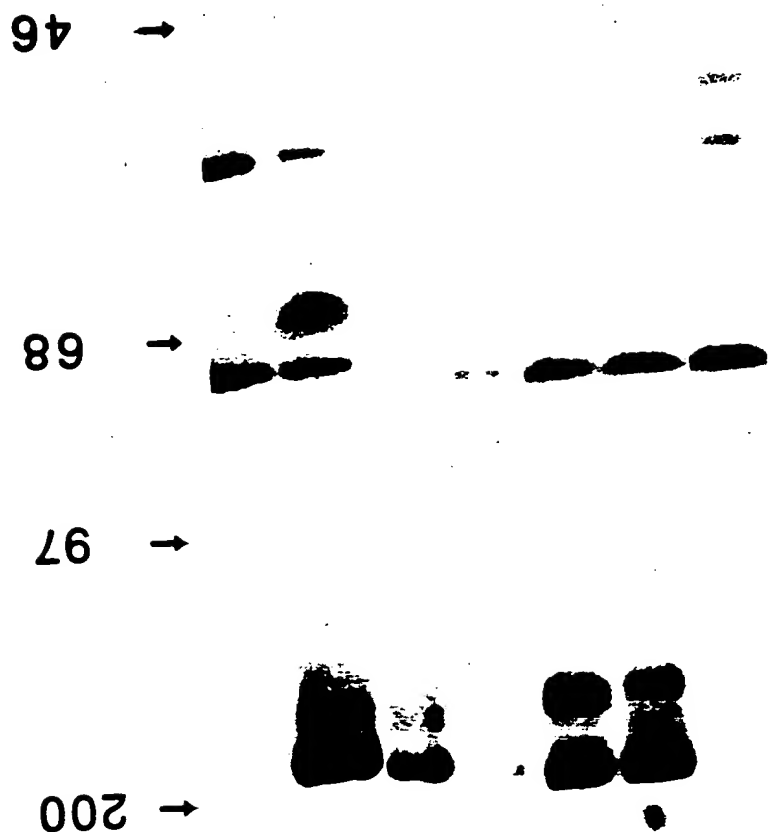




Figure 9





MCF-7  
 MDA-MB361  
 SK-BR-3  
 SK-BR-3(10µg)  
 LTR-1/erbB-2  
 LTR-2/erbB-2  
 NIH/3T3

Figure 10